Scoring table:

Database :

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Human DNA

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Homo sap Sesamum

Homo HOMO

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                                                                                                                                                              AC090843 Mus muscu
AX089374 Sequence
AF013235 Quiscalus
AB067610 Ophthalmo
                                                                                             AC018496 Homo sapi
AC0276190 Homo sapi
AC027763 Homo sapi
AC040977 Homo sapi
AC081492 Homo sapi
AC087090 Homo sapi
AC073565 Mus muscu
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Linaceae; Linum.
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AC007915 Genomic s
AL161627 Human DNA
AC011059 Homo sapi
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AL121875 Human DNA
AC079089 Homo sapi
AC018791 Homo sapi
AL354717 Homo sapi
AL671890 Mus muscu
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Chaudhary, S., van Rooijen, G., Moloney, M.M. and Singh, S. Flax seed specific promoters
Patent: Wo 0116340-A 8 08-WAR-2001;
SembioSys Genelics Inc. (CA); COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION (AU)
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AB017353 I
AC010504 AC101305 A
AC101138 AC101138 AC004500 I
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Copyright (c) 1993 - 2000 Compugen Ltd.
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4381 cggacgtaagggtggntgtcgacgtcntcgtttcnggaggcgnattcatgaagggttaaa 4440
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* (see http://www.hgsc.bcm.tmc.edu/docx/Genbank_draft_data.html).

* NOTE: This is a 'working draft, sequence. It currently

* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* is not known and their order in this sequence record is

* arbitrary daps between the contigs are represented as

* truns of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
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Consensus quality: 15808 bases at least Q30
Consensus quality: 17668 bases at least Q20
Estimated insert size: 10184; sum-of-contigs estimation
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1929: gap of unknown length
3748: contig of 1819 bp in length
3848: gap of unknown length
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AC108615 113725 bp DNA linear HTG 31-JAN-2002 Rattus norvegicus clone CH230-290E9, *** SEQUENCING IN PROGRESS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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* (see http://www.hqsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 62 contigs. The true order of the pieces

* sonk known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submission
Submitted (31-3AN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 87886 bases at least Q40 consensus quality: 94485 bases at least Q30 consensus quality: 99429 bases at least Q30 Estimated insert size: 82890; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
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Sequencing vector: Plasmid: M77789
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329First call to findPhrapList
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3973: contig of 3973 bp in length
4073: gap of unknown length
7436: contig of 3363 bp in length
7536: gap of unknown length
10805: contig of 3269 bp in length
10905: gap of unknown length
13707: contig of 2802 bp in length
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Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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Submitted (20-001-2001) Sanger Centre, Hinxton, Cambridgeshire, Calbnitted (20-001-2001) Sanger Centre, Hinxton, Cambridgeshire, Callo 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone of 24, 2001 this sequence version replaced gi:15131189.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations to the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a mail overlap as described above.

This sequence was finished as follows unless otherwise noted: all
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Human DNA sequence from clone RP11-9E13 on chromosome 10, complete
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Mammalia; Eutheria; Primates; Catarrhini; Kominidae; Homo.
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Direct Submission
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                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl0
RRP1-9E13 is from the library RPC1-11.1 constructed by the group of Pittp://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RP11-9E13 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP11-9E13 is at 138733 in this sequence. The true right end of clone RP11-9E13 is at 2000 in
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/note="Single clone region. Assembly confirmed by
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/note="Single clone region. Assembly confirmed by
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artificial sequence.
1 (bases 1 to 32)
Chaudhary, S., van Rooijen, G., Moloney, M.M. and Singh, S.
Flax seed specific promoters
Patent: WO 0116340-A 22 08-MAR-2001:
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/db_xref="taxon:32630"
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/evidence=not_experimental
29780 c 28584 g 37089 t
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Sequence 22 from Patent W00116340.
AX089372
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127610. .128010
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                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
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55963. .56014
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62420. .63555
/note="CpG island"
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100.0%; Pre
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Matches 25; Conservative
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/Translation="MALTSLLSFFIVVTLLIRGLSAQLAGEQDFYWQDLQSQQQHKLQ
ARTDGRVERLTAQEFTIRFESEAGLTEFWDRNNQFECAGVAAVRNIQPRGLLLPHY
NNAPQLLYVVRGRGIQGTYPECAETFERDTOPRAPROPRAFKYRGFRQGTLA
LPAGITLMFYNNGGEPLITVALDTGNAAMOLDQTRHFFLAGNPGGRQSYFGRPQT
EKQQGFTKNIFNGFDDEILADARGVDVQTARRLKGQDDLRGRIVRAERLDIVLPGEEE
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VPQNYVVAKRASQDEGLEWISFKTNDNAMTSQLAGRLSAIRAMPEEVVMTAYQVSRDE
ARRLKYNREESRVFSSTSRYSWPRSSRPMSYMPKPFEYVLDVIKSMM"
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Homo sapiens chromosome 3 clone RP11-710E4 map 3p, WORKING DRAFT
PLN 02-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biotechnology, National Chung-Hsing University, Taichung 40227,
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Submitted (01-MAR-2000) Graduate Institute of Agricultural
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AF240004 1683 bp mRNA linear Sesamum indicum 11S globulin mRNA, complete cds.
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ACCESSION

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VERSION SOURCE REFERENCE AUTHORS

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contig of 5051 bp in length
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gap of unknown len
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gap of unknown len
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gap of unknown 1
contig of 3428 b
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of 2248
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114393: gap of unknown
  contig of 1456
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gap of unknown
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gap of unknown
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

I (Dases 1 to 133108)

Bao.J., Bao.Q., Bao.W., Bian.X., Cao.T., Chen.C., Chen.J., Ding, H., Dong, W., Fan, H., Feng, X., Gau.D., He.L., Hu.S., Li, Y., Kang, X., Gao.D., He.L., Hu.S., Li, S., Li, T., Liu, Y., Liu, N., Liu, S., Li, C., Li, G., Li, G., Li, G., Li, G., Li, G., Li, G., Li, C., Li, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (05-APR-2000) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beljing, Beljing
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On May 29, 2000 this sequence version replaced gl:7417469.
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Sequencing vector: pCUG18; 100% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 110057 bases at least Q40
Consensus quality: 124151 bases at least Q30
Consensus quality: 133102 bases at least Q20
Insert size: 102269; sum-of-contigs
Quality coverage: 3.16x in Q20 bases; sum-of-contigs
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Center clone name: RP11-710E4
SEQUENCE, 38 unordered pieces.
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Center code:Beijing
Website:http://hgc.iqtp.ac.cn
http://www.genomics.org.cn
                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT
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                                          AC034196.2 GI:8101269
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                        AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 24; DB 2; Length 133108;
100.0%; Pred. No. 0.4;
tive 0; Mismatches 0; Indels 0;
                         4065, 5164 "assembly_name:Contig27" /note="assembly_name:Contig20" 5265, 6462 /note="assembly_name:Contig23" 6563, 7875
 7976. .9431
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9532. .11077
/note="assembly_name:Contig29"
11178. .12990
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17170. .18806
                                                                                                                                                                                                                                                               17170. 18806
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18907. .20498
7006e="assembly_name:Contig35"
20599. .23090
7006e="assembly_name:Contig36"
23191. .26302
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35671, .37854
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39305, 42732
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42833. .45249
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48785. 52145
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/note="assembly_name:Contig32"
15335. .17069
                                                                                                                                                                                                                                                                                                                                       23191. .26302
/note="assembly_name:Contig37"
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28934. 31329
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/note="assembly_name:Contig40"
33323. .35570
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45350. .48684
'note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig39"
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56038. .59494
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June 1995 1 to 148598)

DOE Joint Genome Institute.

DOE Joint Genome Institute.

DoE Joint Genome Institute.

Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:7711677.

----Genome Center

Center: Joint Genome Institute
Center Code: JGI
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Consensus quality: 144004 bases at least Q30
Consensus quality: 145802 bases at least Q30
Consensus quality: 145802 bases at least Q30
Estimated insert size: 176000; pulse field gel estimation
Estimated insert size: 147698; sum-of-contigs estimation
Quality coverage: 5.34 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 20 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148598)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
the accession number will be preserved.
1 5195: contig of 5195 bp in length
5196 5295: gap of unknown length
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contig of 17320 bp in length
gap of unknown length
contig of 1050 bp in length
gap of unknown length
contig of 9884 bp in length
gap of unknown length
contig of 8945 bp in length
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gap of unknown length
contig of 4122 bp in length
gap of unknown length
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gap of unknown length
contig of 6150 bp in length
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                                                                                             Sequencing of Human Chromosome
Unpublished
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhin; Hominidae; Homo.

1 (bases 1 to 152602)
Bao, V., Bao, W., Bian, X., Cao, T., Chen, C., Chen, J., Ding, H.,
Bong, W., Fan, H., Feng, X., Guan, Q., Gu, X., Guo, D., He, L., Hu, S.,
Huang, F., Jin, Y., Kang, N., Li, C., Li, C., Li, G., Li, J., Li, L.,
Li, S., Li, T., Liu, Y., Liu, N., Liu, M., Liu, Y., Li, W., Li, W.,
Luo, J., Niu, Y., Qi, Q., Qi, X., Song, S., Sun, M., Sun, Y.,
Luo, J., Wang, X., Wang, J., Wang, J., Wang, L., Wang, L., Wang, R.,
Wang, X., Wang, Y., Wu, D., Wu, Q., Xie, F., Xuan, Z., Xue, Y.,
Yan, C., Yang, X., Yu, B., Zeng, Y., Zhang, L., Zhang, H., Zhang, H.,
Zhang, L., Zhang, M., Zhang, X., Zhang, Y., Zhang, Y.,
Zhang, Z., Zhu, B., Yu, J. and Yang, H.,
Chromosome 3p genomic sequence
AL Onpublished
Chromosome 3p genomic sequence
Sun, W., Hu, S., Dong, W., Wang, H., Xang, X., Cheng, C., Wang, Y.,
Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Zhang, Y., Zhang, Y.,
Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, X., Zhang, M., Li, L., Feng, X., Yu, J.,
and Wang, H., Zhang, H., Liu, N., Wu, D., Yu, B., Zhang, M., Li, L., Feng, X., Yu, J.,
and Wang, M., Zhang, M., Zhang, M., Li, L., Feng, X., Yu, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC026193 152602 bp DNA linear HTG 29-MAY-2000 Homo sapiens chromosome 3 clone RP11-416H8 map 3p, WORKING DRAFT SEQUENCE, 57 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                           /clone_"CTB-43D14"
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41000 a 35188 c 33298 g 37210 t 1902 others
146683: contig of 7608 bp in length

14783: gap of unknown length

14 148598: contig of 1815 bp in length

Location/Qualifiers
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Sequencing vector: pdC18; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye, 45% of reads
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                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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Center clone name: RP11-416H8
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http://www.genomics.org.cn
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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nes 24; Conserv
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146784
         139076
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently 
* consists of 57 contigs. The true order of the pieces 
* is not known and their order in this sequence record is
         Assemily projumer, filely, terror of the consensus quality: 115486 bases at least Q40 consensus quality: 144075 bases at least Q30 consensus quality: 181307 bases at least Q20 Insert size: 86668; sum-of-contigs Quality coverage: 3.78x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                               1540: contig of 1540 bp in length
1640: gap of unknown length
2835: contig of 1195 bp in length
                                                                                                                                                                                                                                                                                                                                                   unknown length
of 1626 bp in length
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/note="assembly_name:Contig42"
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/note="assembly_name:Contig46"
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/note="assembly_name:Contig51"
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gap of unknown
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E (Dases 1 to 162433)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barnah. N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewarn, C., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHubh, W., Forrest, C., Gage, D., Gradapan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Kalein, J., Langocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meltin, J., Meneus, L., Mihova, T., Miradad, C., O'Neni, D., O'Neil, D., Olivar, T. M., Peterson, K., Pierre, N., Pierre, M., Sanico, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Fravers, M., Trigillo, J., Yassiliev, H., Yael, R., Vo, A., Halson, B., Stanger, H., Yael, R., Vo, A., Halson, B., Man, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACU243/7 162433 bp DNA linear HTG 26-MAY-2000
Homo sapiens clone RPI1-611H22, WORKING DRAFT SEQUENCE, 24
unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162433)
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All repeats were identified using RepeatMasker: smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Sequencing vector: M13; M77815; 100% of reads
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Unpublished
                            8532. .10150
/note="assembly_name:Contig62"
10251. .11827
/note="assembly_name:Contig57"
                                                                                    10251. .11827
/note="assembly_name:Contig63"
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clone_end:T7

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arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                             Quality coverage: 3.3 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
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93418: contig of 11503 bp in length
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93519 107008: contig of 13490 bp in length
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71201: contig of 10114 bp in length
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16603 19777: contig of 3175 bp in length
19778 19877: gap of 100 bp
19878 23124: contig of 3247 bp in length
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Consensus quality: 147711 bases at least Q40 Consensus quality: 155048 bases at least Q30 Consensus quality: 158115 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 160133; sum-of-contigs
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contig of 2333 bp in length
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28282: contig of 5058 bp in length
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="assembly_fragment"
13945. .16502
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/note="assembly_fragment"
71302. .81815
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/note="assembly_fragment"
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143809. .162433
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19878. .23124
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37580. 44685
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44786. 52369
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31844. .37479
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2774. .5106
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Best Local Similarity 100.(
Matches 24; Conservative
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KEYWORDS
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http://www.genomics.org.cn
Contact:hgc@igtp.ac.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: RP11-372K9
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                                                                                                                                                                REFERENCE
                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (13-DEC-1999) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing,
100101, P.R.China
On Jan 9, 2000 this sequence version replaced gi:6563492.
* NOTE: This is a "working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
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1 (Dases 1 to 165077)
Bao,J., Bao,D., Bao,M., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H., Dong,W., Fan,H., Feng,X., Guan,Q., Gu,X., Guo,D., He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,G., Li,J., Li,L.,
1 (bases 1 to 163272)
Bao,J., Hu,S., Dong,W., Zhang,X., Wang,J., Zhang,Y., Zhang,H.,
Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y.,
Niu,Y., Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H.,
Liu,Y., Li,G., Li,C., Bao,Q., Wang,X., Wang,X., Song,L., Zhang,L.,
Guo,D., Huang,F., Zhang,G., Li,J., Bian,X., Zhang,M., Li,L.,
Feng,X., Yu,J. and Yang,H.
                                                                                                                                                                              Li,T., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B., Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y., Qi,X., Yang,Y., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y., Li,G., Li,C., Bao,Q., Bao,Q., Wang,X., Song,L., Zhang,L., Guo,D., Huang,F., Zhang,G., Li,J., Blan,X., Zhang,M., Li,L., Feng,X., Yu,J.
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gap of unknown length
26723: contig of 21882 bp in length
gap of unknown length
57119: contig of 30396 bp in length
gap of unknown length
104873: contig of 47754 bp in length
gap of unknown length
gap of unknown length
163272: contig of 58399 bp in length.
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/clone="RP11-210B17"
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AC026190.2 GI:8101204
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                         and Yang, H.
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JOURNAL
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     REFERENCE
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                        AUTHORS
                                                                                                                                                 JOURNAL
                                                                                                                                                                                   AUTHORS
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LOCUS

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2 (bases I to 165077)
Sun,W., Hu,S., Dong,W., Wang,J., Zhang,Y., Zhang,H., Liu,B.,
Bao,W., Sun,Y., Wu,Q., Wang,H., Yang,X., Cheng,C., Wang,Y., Niu,Y.,
Qi,X., Li,T., Zhang,H., Liu,N., Wu,D., Yu,B., Fan,H., Liu,Y.,
Li,G., Bao,Q., Bao,J., Wang,X., Song,L., Zhang,L., Guo,D.,
Huang,F., Zhang,G., Li,J., Błan,X., Zhang,M., Li,L., Feng,X., Yu,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-MAR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
Li,S., Li,T., Liu,Y., Liu,N., Liu,B., Liu,Y., Li,W., Li,W., Li,Y.,
Luo,J., Niu,Y., Qi,Q., Qi,X., Song,S., Sun,M., Sun,W., Sun,Y.,
Tao,R., Wang,H., Wang,J., Wang,L., Wang,L., Wang,L., Wang,X.,
Wang,X., Wang,Y., Wu,Q., Xie,F., Xuan,Z., Xua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100101, P.R.China
On May 29, 2000 (1915) sequence version replaced gi:7272007.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality coverage: 3.38x in Q20 bases; sum-of-contigs
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Sequencing vector: pUG18; 100% of reads
Chemistry: Dye-terminator: ET 5% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 151327 bases at least 040
Consensus quality: 159291 bases at least 030
Consensus quality: 16481 bases at least 020
Insert size: 156591; sum-of-contigs
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us-09-645-593-8.rge

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barra, N., Bastien, V., Beda, F., Bouknaller, B., Brown, A., Burkett, G., Beda, F., Boyuslaukiy, L., Bouknalalter, B., Brown, A., Burkett, G., Brown, A., Burkett, G., Brown, A., Burkett, G., Campoptano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, R., Hewland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, R., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McDean, P., McGurk, M., McRenran, R., McGurk, J., McCarthy, M., McDean, P., McGurk, J., Mranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, R., O'Connor, P., O'Neil, D., O'Neil, D., Sautos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Vabramanian, A., Trigilio, J., Young, G., Zahnoun, J., Zimmer, A. and Zody, M., Trigilio, J., Young, G., Submission
                                                                         PRI 01-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (NI-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jan 10, 2002 this sequence version replaced gi:15422062. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 169770)
                                                                                 Homo sapiens chromosome 17, clone RP11-530N7, complete sequence.
AC027763
                                                                           linear
                                                                                                                                                                                                                                                     Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-530N7 Unpublished
                                                                           169770 bp
                                                                                                                                 AC027763.9 GI:18104884
                                                                                                                                                                                                                                                                                                                        (bases 1 to 169770)
                                                                                                                                                                                         Homo sapiens
                                                                           AC027763
                                       RESULT 13
AC027763/c
                                                                                             DEFINITION
                                                                                                                                                                                         ORGANISM
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                                                                                                                 ACCESSION
                                                                                                                                                     KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                   VERSION
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contig of 10027 bp in length
gap of unknown length
contig of 11726 bp in length
gap of unknown length
contig of 12313 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1844 others
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                                                                                                             contig of 10430 bp in length
gap of unknown length
contig of 14524 bp in length
gap of unknown length
                                                                                                                                                                                   135218: contig of 18096 bp in length
135318: gap of unknown length
165077: contig of 29759 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contigl2"
15293 ...20869
16293 ...20869
20970 ...27390
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27491 ...35391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35492. 42412
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/note="assembly_name:Contigl7"
50895. 57502
/note="assembly_name:Contigl8
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/note="assembly_name:Contig11"
10892. 15192
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79556. .91868
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                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_name:Contig6"
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/note="assembly_name:Contig8"
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/note="assembly_name:Contig9"
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100.0%; Pred. No. c...
0; Mismatches
                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                          /clone="RP11-372K9"
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                                                                                                                                                                                                                                                                                                                        /chromosome="3"
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117022: 0
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91868:
91968:
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Best Local Similarity 100.8
Matches 24; Conservative
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Center: Whitehead Institute/ MIT Center for Genome Research
              /".clone="RP11-530N7"
/clone_lib="RPCI-11 Human Male BAC"
complement(1 .321)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Tigger3(Golem)"
complement(6616..6917)
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complement(7109. .7404)
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complement(7688. 8054)
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/db_xref="taxon:9606"
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ement(??o.
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complement(8079..8316)
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complement(8647..9092)
                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="MIR" 715. .2005
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complement(4565. .4630)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2140. .2448)
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                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich"
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046. .6092
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918. .7108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Alusg"
5736. 6015
                                                                                                                     Location/Qualifiers
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                                                                                                                                                                             /chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                        complement(1437.
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AC040977 173878 bp DNA linear HTG 05-SEP-2001
Homo sapiens chromosome 17 clone RP11-589P10 map 17, *** SEQUENCING
IN PROGRESS ***, 7 unordered pieces.
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100.0%; Pred. No. 0.4;
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                                                                                                                                                                                                                                                                                                                                                         /rpt_family="Alusx"
complement(12803, .13403)
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complement(13395, .13500)
/rpt_family="L1M1"
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Best Local Similarity 100.0%; Pred. No. v..
Ameriative 0; Mismatches
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complement(18839, .19064,
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:Omplement'11...
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                                                                                                                                                                                                                                                                                           'rpt_family="(ATG)n"
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complement(9094..99
                                                       /rpt_family="Alusg"
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11116. .11
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AC040977
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/db_xref="taxon:9606"
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Streen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastie, N., Bastie, P., Boda, F., Bodukhgalter, B., Brown, A., Burkett, G., Cooke, P., DeArellano, K., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Rerias, P., FitzHuph, W., Gage, D., Grand-pierre, N., Grand, G., Hagos, B., Heaford, A., Horton, L., Karatas, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lowinson, R., Jones, C., Kann, L., Landers, R., Landers, T., Landers, R., Mclein, J., McGerlan, K., McRernan, K., Morheeters, R., Meldrim, J., Meneus, L., Mihova, T., Mirada, C., Mlenga, V., Morrow, J., Willim, J., Meneus, L., Mihova, T., Mirada, C., Mlenga, V., Morrow, J., Willim, J., Meneus, L., Mihova, T., Mirada, C., Mlenga, V., Morrow, J., Willin, J., Meneus, L., Willow, J., Deterson, K., Pierre, N., Fisani, C., Pollara, V., Raymond, C., Riley, R., Espence, N., Trigillio, J., Vessiliev, H., Viel, R., Schauer, S., Severy, P., Spencer, B., Spencer, S., Severs, R., Schauer, S., Severy, P., Spencer, Submission

Direct Submission

All repeats were identified using Repeatmasker:

Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 5, 2001 this sequence version replaced gi:14336616.

All repeats were identified using Repeatmasker:

Conter, Whitehead Institute/ MIT Center for Genome Center.

Conter, Whitehead Institute/ MIT Center for Genome Center.
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L9393
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116695 132759: contig of 16065 bp in length
118695 132859: gap of 100 bp
132860 173878: contig of 41019 bp in length.
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                            AC040977.5 GI:15431174
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                  Birren, B., Linton, L., Musbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-589P10 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
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/organism="Homo sapiens"

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Direct Submission

Ly Submitted (05-APR-2000) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing 100101, P.R.China

2 (bases 1 to 776217)

3 (bases 1 to 776217)

Bao, O. Bao, W. Bian, X., Cao, T., Chen, C., Chen, J., Ding, H., Dong, W., Fan, H., Feng, X., Gong, J., Guan, Q., Gu, X., Guo, D., Guo, Z., He, L., Huss, Hanang, F., Jin, Y., Liu, Y., Liu, Y., Liu, R., Li, M., Li, Li, S., Li, T., Li, Y., Liu, Y., Liu, B., Liu, Y., Liu, M., Li, M., Li, M., Li, Song, L., Song, S., Sun, M., Sun, W., Sun, Y., Tao, X., Tao, R., Wang, M., Wang, J., Wang, J., Wang, L., Wang, R., Wang, X., Wang, Y., Wu, D., Wu, O., Xie, F., Xuan, Z., Xue, Y., Yan, C., Yang, X., Yu, B., Zahang, X., Zhang, X., Zhu, B., Zhu, N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 176217) (Ariong, H., Zhou, Y., Dong, H., Lin, W., Chen, B., Zhang, C., Zhang, Y., Cai, Z., Ying, H.F., Wang, H., Gu, W., Zhu, G., Tu, Y., Zhang, X., Jia, J., Shen, H., Zhang, D., Wu, C., Lu, G., Zhong, M., Jiang, H., Ren, S., Fu, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI 11-FEB-2001
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Homo sapiens chromosome 3 clone RP11-416N8 map 3p, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                         Score 24; DB 2; Length 173878;
Pred. No. 0.4;
                                                                                                                                                                                            685 others
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                                                                                                                               /clone_lib="RPCI-11 Human Male BAC" 49141 a 39705 c 39091 g 45256 t 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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Unpublished
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http://www.genomics.org.cn
                                                                                           /clone="RP11-589P10"
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/chromosome="17"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.5%; Scc
Best Local Similarity 100.0%; Pa
Matches 24; Conservative 0;
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AC034192.4 GI:12745080
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Center clone name: RP11-416NB Sequencing vector: p0CNB 100% of reads chemistry: Dye-terminator: ET 55% of reads consensus quality: 179310 bases at least Q20 consensus quality: 179518 bases at least Q20 insert size: 176217; sum-of-contigs consensus quality: 179518 bases at least Q20 consensus quality: 179518 bases sum-of-contigs in the conformal size: 10.6%; sum-of-contigs cource //db_xref="taxon'/qualifiers" //db_xref="taxon'/qualifiers" //db_xref="taxon'/qualifiers" //db_xref="taxon'/qualifiers" //db_xref="taxon'/qualifiers" //db_xref="taxon'/qualifiers" //db_xref="taxon'/qb," //dbo=""RP11-416NB" //db," //dbo=""RP11-41
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